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# Contrasting responses of soil respiration and temperature sensitivity to land use types: Cropland *vs.* apple orchard on the Chinese Loess Plateau

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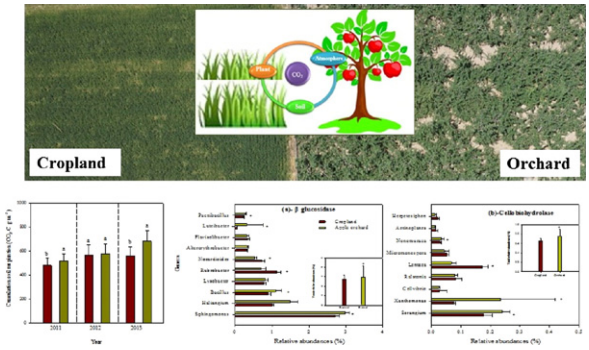
## HIGHLIGHTS

- Contrasting responses of soil respiration and $Q_{10}$ to land use types in fragmented Loess Plateau
- Compared to the cropland, the lower $Q_{10}$ in the apple orchard resulted from varied bacterial community structure and β-glucosidase and cellobiohydrolase activity.
- Lower C: N ratios in the apple orchard possibly contributed to its lower $Q_{10}$.

## GRAPHICAL ABSTRACT

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## ABSTRACT

Land use plays an essential role in regional carbon cycling, potentially influencing the exchange rates of $CO_2$ flux between soil and the atmosphere in terrestrial ecosystems. Temperature sensitivity of soil respiration ($Q_{10}$), as an efficient parameter to reflect the possible feedback between the global carbon cycle and climate change, has been extensively studied. However, very few reports have assessed the difference in temperature sensitivity of soil respiration under different land use types. In this study, a three-year field experiment was conducted in cropland (winter wheat, *Triticum aestivum* L.) and apple orchard (*Malus domestica* Borkh) on the semi-arid Loess Plateau from 2011 to 2013. Soil respiration (measured using Li-Cor 8100), bacterial community structure (represented by 16S rRNA), soil enzyme activities, and soil physicochemical properties of surface soil were monitored. The average annual soil respiration rate in the apple orchard was 12% greater than that in the cropland (2.01 *vs.* 1.80 μmol $m^{-2}$ $s^{-1}$), despite that the average $Q_{10}$ values in the apple orchard was 15% lower than that in the cropland (ranging from 1.63 to 1.41). As to the differences among predominant phyla, Proteobacteria was 26% higher in the apple orchard than that in the cropland, whereas Actinobacteria and Acidobacteria were 18% and 36% lower in the apple orchard. The β-glucosidase and cellobiohydrolase activity were 15% (44.92 *vs.* 39.09 nmol $h^{-1}$ $g^{-1}$) and 22% greater (21.39 *vs.* 17.50 nmol $h^{-1}$ $g^{-1}$) in the apple orchard than that in the cropland. Compared to the cropland, the lower $Q_{10}$ values in the apple orchard resulted from the variations of bacterial community structure and β-glucosidase and cellobiohydrolase activity. In addition, the lower C: N ratios in the apple orchard (6.50 *vs.* 8.40) possibly also contributed to its lower $Q_{10}$ values. Our findings call for further studies to include the varying effects of land use types into consideration when applying $Q_{10}$ values to predict the potential $CO_2$ efflux feedbacks between terrestrial ecosystems and future climate scenarios.



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## 1. Introduction

Soil respiration is a key component of terrestrial carbon cycling (Raich and Schlesinger, 1992; Cox et al., 2000; Jiang et al., 2015). A small variation in temperature sensitivity of soil respiration (often expressed as $Q_{10}$) can cause a large bias in predicting soil $CO_2$ release into the atmosphere, especially under the ever-changing climate conditions in the future (Xu and Qi, 2001; Wang et al., 2016). Long-term erosion and intensive cultivation has incised the vast Loess Plateau in China into fragmented tableland, slopes or gullies, and valley bottoms (Wang et al., 2017a, 2017b). In order to tackle such soil erosion problems, the "Grain-for-Green" rehabilitation project was initiated in 1980s, which converted all cropland on slopes steeper than 25° to orchard, forest or grassland (Deng et al., 2014). This consequently formed complex combinations of tableland, slopes and valleys with cropland, grassland, orchard and woodland. Therefore, it becomes critically essential to systematically investigate the effects of land use on $Q_{10}$ values in the context of complex landforms so as to better understand the role of soil respiration in the carbon cycling on the fragmented Loess Plateau.

In general, land use conversion alters vegetation coverage, soil physicochemical and microbial properties, which all affect soil respiration (Iqbal et al., 2008; Liu et al., 2008; Javed et al., 2010; Kreba et al., 2013; Wang et al., 2016). For instance, soil respiration can vary among crop species and root biomass amount under different land use types (Lee and Jose, 2003; Raich and Tufekcioglu, 2000; Wang et al., 2016). Even after excluding the variation of root effects, soil respiration can also differ among land use types because of different redistribution of precipitation and solar radiation by vegetation canopy (Bryant et al., 2005; Dan and Giardina, 1998; Smith and Johnson, 2004; Raich and Tufekcioglu, 2000; Ritter et al., 2005; Rutter and Morton, 1977). Furthermore, soil respiration can also change with soil microbial community structure (Asgharipour and Rafiei, 2011; Wallenius et al., 2011; Moon, 2016; Zhang et al., 2016a, 2016b), and soil C-degrading extracellular enzymes *via* secreting by soil microbes (Allison and Vitousek, 2004; Davidson and Janssens, 2006; Burns et al., 2013; Wang et al., 2017). The quantity and stability of substrate under different land use types was another factor influencing soil respiration, as better availability of carbon was reported to produce greater soil respiration (Allison et al., 2014; Fang et al., 2014; Ferreira et al., 2016).

Since $Q_{10}$ represents the sensitivity of soil respiration to temperature changes, all the above-mentioned factors can also cause variation in $Q_{10}$ values. In general, $Q_{10}$ values tends to increase with decreasing soil temperature and increasing moisture (Kirschbaum, 1995; Qi and Xu, 2001; Janssens and Pilegaard, 2003), both of which are essential environment factors for soil microbial growth, community structure and activity (Avrahami et al., 2003; Brockett et al., 2012; Ren et al., 2017; Supramaniam et al., 2016). Similarly, $Q_{10}$ values can also be influenced by the quality of substrate (Conant et al., 2008; Karhu et al., 2010; Conant et al., 2011), as the degradation of low-quality substrate, which has higher total activation energy for microorganism decomposition, has a higher $Q_{10}$ values than simple base on enzyme-kinetic hypothesis (Bosatta and Agren, 1999; Wang et al., 2017a, 2017b). This further suggests that soil nutrient can also influence $Q_{10}$ values by altering the stability of substrate (*e.g.* C: N ratio) (Pregitzer et al., 2000; Leifeld and von Lutzow, 2014). However, very few studies have dedicated to investigate the effects of soil bacterial community structure to soil respiration and $Q_{10}$ values under different land use types.

In this study, the potential effects of soil bacterial community on soil respiration and $Q_{10}$ values were compared between soils from an apple orchard and a cropland on the Chinese Loess Plateau. We hypothesized that different land use types would affect all the above-described factors, which in turn would lead to changes in soil respiration and its sensitivity to temperature changes. Therefore, the aims of this study are to: 1) compare the difference of soil respiration and $Q_{10}$ values between cropland and apple orchard; 2) characterize the changes in bacterial community and soil extracellular enzymatic activity under different land use types; and 3) explore the potential effects of bacterial community and activities on $Q_{10}$ values and soil respiration under different land use types.

## 2. Materials and methods

### 2.1. Study site

The study site is located in a typical tableland-gully region of southern Loess Plateau in the middle reaches of Yellow River (35°13′N, 107°40′E; 1220 m a.s.l) in Wangdonggou Catchment, Changwu Country, Shaanxi Province, China (Fig. 1). It has a continental monsoon climate characterized by a seasonal monsoon rhythm with hot summers and cold winters. The annual mean precipitation is 560 mm, 60% of which occurs between July and September. The annual mean air temperature is 9.4 °C, and ≥10 °C accumulated temperature is 3029 °C. The annual sunshine hours are 2230 h, annual total radiation is 484 kJ $cm^{-2}$, and frost-free period is 171 days. The soil at the study site is a uniform loam of loess deposits that belongs to Cumulic Haplustolls according to the American system of soil classification, originated from the parent material of calcareous loess (Wang et al., 2016). All meteorological data during experiment time were provided by Changwu State Key Agro-Ecological Experimental Station (Fig. 2).

### 2.2. Different land use types

Two ecosystem, apple orchard and cropland, with different agronomic management practices were selected. The apple orchard investigated in this study was dominated by Fuji apple trees (*Malus domestica* Borkh), and the cropland was 0.5 km away from the apple orchard and planted with winter wheat (*Triticum aestivum* L., cv. Changwu 89 (1) 3–40). The detail agronomic management practices were listed in Table 1.

On the cropland, three plastic collars (20 cm in diameter × 12 cm in height) were inserted 2 cm into the soil in a complete randomized block design. In the apple orchard, considering the possible spatial variation, it was divided into trisections along diagonal. In each section, a well-grown apple tree with no diseases or insect pests was selected. At different distances (0.5 and 2 m radial distance) from each tree trunk, plastic collars were inserted into the soil in three different directions (0°, 120°, and 240°).

### 2.3. Measurements of soil respiration, soil temperature and moisture

Soil respiration was measured every 15 days from March 2011 to November 2013, from 09:00 am to 11:00 am on each measurement day (Javed et al., 2010). During December, January and February, due to cold weather which could inhabit root and microbial activity, no measurements were carried out. The soil respiration rates were determined using an automated and closed soil $CO_2$ flux system equipped with a portable chamber of 20 cm in diameter (Li-8100, Lincoln, NE, USA). Before each measurement, all visible living organisms were manually removed.

Soil temperature (three measurements per collar) and moisture (four measurements per collar) were measured 10 cm away from the chamber collar at the same time with the soil respiration. Soil temperature was measured using a Li-Cor thermocouple probe and soil moisture at 5 cm depth was recorded by a Theta Probe ML2X with an HH2 moisture meter (Delta-TDevices, Cambridge, England). Soil water-filled pore space (WFPS) was converted from following equation: WFPS (%) = [volumetric water content / 100 × (2.65 − soil bulk density) / 2.65] (Ding et al., 2007).

### 2.4. Sampling and analysis

Three cropland soil samples (0–20 cm) were collected using a soil auger of 3 cm in diameter in 28 September 2013 (the last experimental

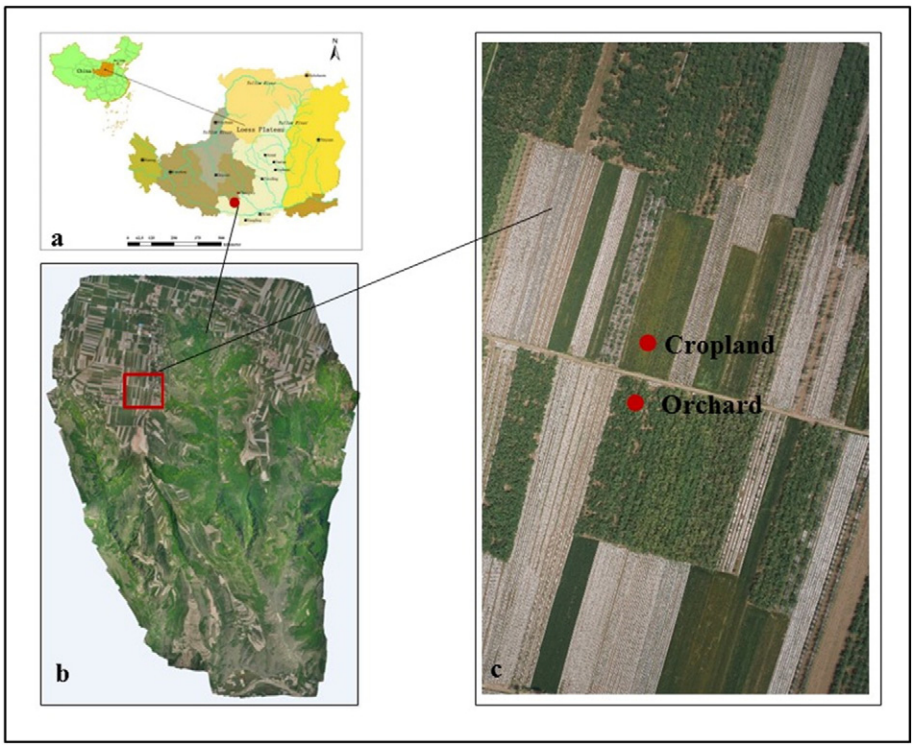


**Fig. 1.** A sketch map of the Loess Plateau, China (Fig. 1-a adopted from Wang et al., 2016).

year). For each cropland soil sample, six different subsamples were collected and subsequently mixed. Similarly, three apple orchard soil samples were collected, given the tree-scale spatial variation, six subsamples were located at the same sites as the plastics collars. Each sample was passed through a 2.0-mm sieve and divided into three subsamples: one part stored at −80 °C for DNA extraction, the second part stored at 4 °C for the measurement of soil microbial biomass carbon (SMBC) and soil enzyme activities, and the third part was air dried and then crushed to pass through a 0.15 mm sieve for soil organic carbon (SOC) measurements. The SOC of each soil sample was determined using the $K_2CrO_7$-$H_2SO_4$ oxidation method (Sparks et al., 1996). The N concentrations were tested by acid digestion following the Kjeldahl method (Grimshaw et al., 1989). The SMBC was measured by the chloroform fumigation-extraction method (van Gestel et al., 2011; Vance et al., 1987). The soil enzyme activities were determined using a microplate fluorimetry method (Trap et al., 2012).

Soil DNA was extracted from 0.5 g soil using the MoBio PowerSoil™ DNA Isolation Kits (Mo Bio Laboratories, Carlsbad, CA, USA) FastDNA® Spin Kit for Soil (MP Biomedicals, Cleveland, OH, USA) according to the manufacturer's instructions. The purified DNA was diluted with 50 μl sterilized water and checked for quality and quantity using a Nanodrop ND-2000 UV-VIS Spectrophotometer (NanoDrop Technologies, Wilmington, DE, USA).

DNA was amplified using the primers 515F (50-GTGCCAGCMGCCGCGGTAA-30) and 806R (50-GGACTACHVGGGTWTCTAAT-30) designed to be universal for bacteria and archaea (Caporaso et al., 2011). Amplification was performed using Thermo Scientific® Phusion High-Fidelity PCR Master Mix (New England Biolabs, UK). After amplification, the obtained products were purified using a Qiagen Gel Extraction Kit (Qiagen, Germany). Sequencing was performed using the Illumina HiSeq2500 platform at Novogene Bioinformatics Technology Co., Ltd., Beijing, China.

All sequence reads were merged using FLASH (Magoč and Salzberg, 2011) and assigned to each sample according to their barcodes. Sequence analysis was performed by UPARSE software package using the UPARSE-OTU and UPARSE-OTUref algorithms (Edgar, 2013). Sequences with ≥97% similarity were clustered into operational taxonomic units (OTUs). The aligned 16S rRNA gene sequences were used for a chimera check using the Uchime algorithm (Edgar et al., 2011). Taxonomy was assigned using the Ribosomal Database Project classifier

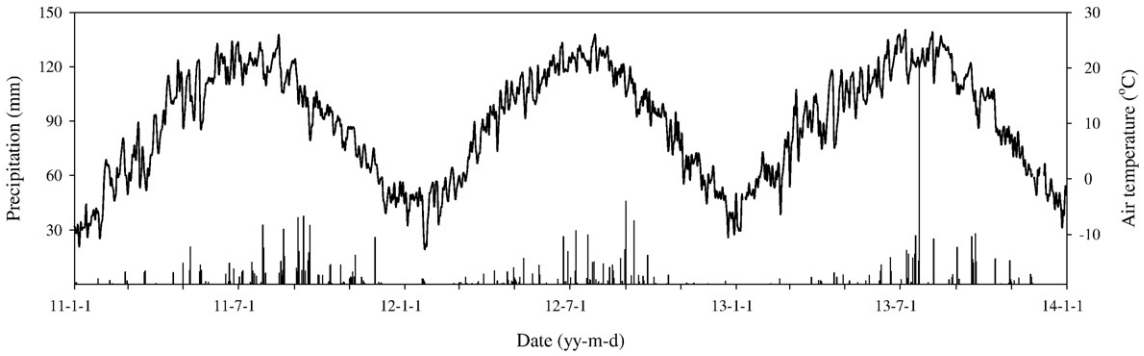


**Fig. 2.** Variation of precipitation (mm) and air temperature (°C) over the experimental period from 2011 to 2013.

**Table 1**
Differences in land management between cropland and orchard in rain-fed ecosystem.

| Ecosystem | Cropland | Orchard |
|---|---|---|
| Vegetation | Winter wheat: *Triticum aestivum* L., cv. Changwu 89 (1) 3–40 | Apple: Fuji apple trees, *Malus domestica* Borkh |
| Planting | Late of September each year, seeding rate of 150 kg $ha^{-1}$ | In 2000, 625 plants $ha^{-1}$ |
| Harvesting | Late June (Grain and aboveground biomass by cutting close to the ground) | Late of September (Fruits) |
| Residue | All harvested biomass was removed from the field | All the litter was removed in autumn, including leaf (Late of October), Pruned branches (Early March), blossom and fruit thinning (April and May) |
| Space distance | 20 cm | 4 m × 3 m |
| Tillage | Prior to sowing | November and late June |
| Fertilization | Broadcasted 5 to 7 days prior to sowing: Top-dressing (160 kg N $ha^{-1}$, 39 kg P $ha^{-1}$) | November: at the depth of 0–50 cm by digging a hole 1 m away from the tree row, 200 kg N $ha^{-1}$, 385 kg P $ha^{-1}$<br>Late June: top-dressing, 100 kg N $ha^{-1}$<br>Late June: Top-dressing (100 kg N $ha^{-1}$). |

(Wang et al., 2007). Each sample was rarefied to the same number of reads (64,246 sequences) for both alpha-diversity (Chao1 estimator of richness, observed species and Shannon's diversity index) analyses. The original sequence data are available at the NCBI with accession number SUB2869376.

### 2.5. Data analysis

A univariate exponential function model was used to characterize the relationship between soil respiration and soil temperature (Davidson et al., 1998):

$$y = \beta_0 e^{\beta 1 T} \quad (1)$$

where $y$ is the measured soil respiration (μmol $m^{-2}$ $s^{-1}$), T is the measured soil temperature (°C) at a certain soil depth.

The $Q_{10}$ values were calculated by Eq. (2) (Xu and Qi, 2001):

$$Q_{10} = e^{10\beta 1} \quad (2)$$

where $\beta_1$ is calculated by Eq. (1).

Alpha diversity (Chao1 estimator of richness, observed species and Shannon's diversity index) was calculated with QIIME (Version 1.7.0). All data (mean ± SD, $n = 3$) were subject to ANOVA, followed by a LSD test for *post hoc* comparisons of means. Statistical significance was defined as $p \le 0.05$. The genera of bacteria (Top 300) which contains the genes encoding the 3.2.1.21 and 3.2.1.91 were selected based on KEGG database (http://www.kegg.jp).

## 3. Results

### 3.1. Soil biochemical properties

Soil biochemical properties varied considerably between the apple orchard and cropland (Table 2). Total N, soil moisture, soil microbial biomass carbon (SMBC), ration of SMBC and SOC (SMBC/SOC), and soil enzyme activity were generally greater in the apple orchard than that in the cropland, whereas cropland had greater SOC concentration and C: N ratios (Table 2). Total N concentration was 20% (1.13 *vs.* 0.94 g $kg^{-1}$), soil moisture 28% (42.00% *vs.* 32.82%WFPS), SMBC 30% (136 *vs.* 105 mg $kg^{-1}$), SMBC/SOC 46% (19 *vs.* 13) higher in the apple orchard than that in the cropland. However, different land use types resulted in a slight decrease in SOC (7.3%, 7.36 *vs.* 7.9 g $kg^{-1}$) and notable decrease in C: N ratios (23%, 6.5 *vs.* 8.4) in the apple orchard when compared to the cropland. The β-glucosidase and cellobiohydrolase activity were 15% (44.92 *vs.* 39.09 nmol $h^{-1}$ $g^{-1}$) and 22% (21.39 *vs.* 17.50 nmol $h^{-1}$ $g^{-1}$) higher in the apple orchard than that in the cropland.

**Table 2**
Soil physical and chemical properties in cropland and apple orchard.

| Soil characteristics | Cropland | Apple Orchard |
|---|---|---|
| Soil temperature (°C) | 15.90 ± 1.96a | 15.40 ± 0.94a |
| Soil moisture (WFPS%) | 32.82 ± 5.49b | 42.00 ± 3a |
| Soil organic carbon (SOC g $kg^{-1}$) | 7.90 ± 0. 4a | 7.36 ± 0.7a |
| Total nitrogen (g $kg^{-1}$) | 0.94 ± 0.05b | 1.13 ± 0.05a |
| Soil microbial biomass carbon (SMBC mg $kg^{-1}$) | 105.04 ± 10.7b | 136.17 ± 35.0a |
| C: N ratios | 8.40 | 6.50 |
| SMBC/SOC | 13 | 19 |
| β-glucosidase (nmol $h^{-1}$ $g^{-1}$) | 39.09 ± 15.73b | 44.92 ± 11.20a |
| Cellobiohydrolase (nmol $h^{-1}$ $g^{-1}$) | 17.50 ± 7.92b | 21.39 ± 8.79a |

Soil temperature at 5 cm depth showed similar seasonal and annual variations in the apple orchard and the cropland (Fig. 3a), which was in good agreement with the variation of air temperature (Fig. 2). The mean soil temperature over the study period was 15.40 °C in the apple orchard and 15.90 °C in cropland (Table 2). Soil moisture at 5 cm depth (Fig. 3b) fluctuated significantly in response to natural precipitation (Fig. 2). The average annual soil moisture over the study period was 42.00% WFPS in the apple orchard and 32.82% WFPS in the cropland (Table 2).

### 3.2. Soil respiration and $Q_{10}$

Soil respiration showed similar seasonal and annual patterns in the apple orchard and the cropland (Fig. 4): increased gradually as the soil temperature raised from March to June, and decreased rapidly as soil temperature declined after October (Fig. 3a). However, numerically, annual soil respiration rate (calculated by averaging the three years) in the apple orchard (2.01 μmol $m^{-2}$ $s^{-1}$) was 12% greater than that in the cropland (1.80 μmol $m^{-2}$ $s^{-1}$) (Fig. 4). The average annual cumulative respiration in the apple orchard (592 $CO_2$-C g $m^{-2}$) was increased 11% than that in the cropland (533 $CO_2$-C g $m^{-2}$) (Fig. 5).

The temperature sensitivity of soil respiration ($Q_{10}$) in the apple orchard, though not constant over years, was in general lower than that in the cropland (Table 3), ranging from 0.06 to 0.42, respectively. The $Q_{10}$ values between the apple orchard and the cropland differed the most in 2012 (1.35 in the apple orchard 1.77 in the cropland), while varied the least in 2011 (1.47 *vs.* 1.53). After averaging the three years, the average annual $Q_{10}$ values in the apple orchard was 15% lower (1.41) when compared with that in the cropland (1.63). $Q_{10}$ values changed from 1.53 in the cropland to 1.47 in the apple orchard in 2011, from 1.77 to 1.35 in 2012, and from 1.58 to 1.41 in 2013, respectively (Table 3).

### 3.3. Composition of bacterial communities

The Chao1 richness, observed species, Shannon's diversity index and OUT numbers were greater in the apple orchard soil than those in the cropland soil (Table 4). Proteobacteria, Actinobacteria and Acidobacteria were the predominant phyla in the apple orchard and the cropland, with the relative abundances of 12–40%. The relative abundance of phylum Proteobacteria (26%), Gemmatimonadetes in

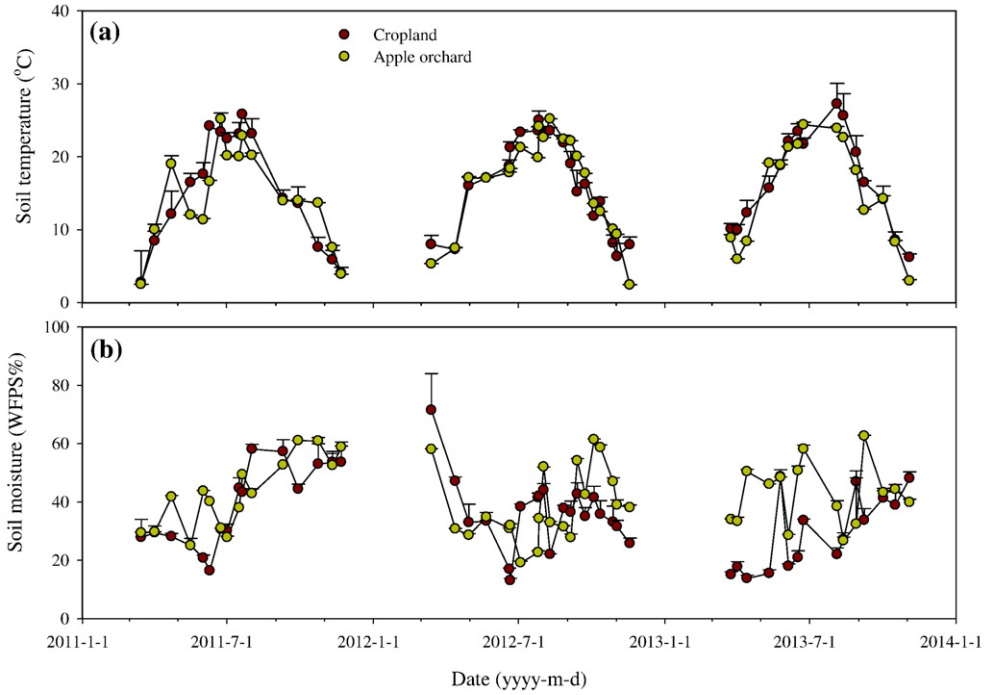


**Fig. 3.** Dynamics of soil temperature (°C) and soil moisture (%WFPS) in the cropland and apple orchard over the experimental period from 2011 to 2013.

the apple orchard was significantly greater (33%) compared with that in the cropland, whereas that of Actinobacteria and Acidobacteria in the apple orchard was 18% and 36% lower than in the cropland (Fig. 6).

The top-10 most abundant classes were significantly different ($p \leq 0.05$) between the apple orchard and the cropland soils (Fig. 6). The abundance of Alphaproteobacteria, Betaproteobacteria, Deltaproteobacteria, Gammaproteobacteria, and Gemmatimonadetes was 10%–60% higher in the apple orchard soil than that in the cropland soil, whereas the abundance of Acidobacteria and Actinobacteria was 44% and 25% lower in the apple orchard soil than that in the cropland soil (Fig. 6).

## 4. Discussion

### *4.1. Changes in soil respiration induced by land use types*

The greater average annual soil respiration in the apple orchard compared to the cropland (by 12%, Figs. 4 and 5) clearly illustrates the effects of land use types to soil respiration. Such responses in soil respiration effects were largely attributed to the following three reasons. 1) While the seasonal patterns of soil respiration (Fig. 4) reflected the regulating effects of soil temperature (Fig. 3a), soil temperature did not contribute much to the difference of soil respiration rates between the two land use types, as the soil temperature was not significantly different between the apple orchard and the cropland (Table 2). 2) The 28% greater soil moisture in the apple orchard probably contributed to its greater soil respiration (Table 2, Figs. 4 and 5). Such differences in soil moisture may not be significant for other ecosystems, but were very likely the limiting factor in physiological processes (Balogh et al., 2011; Cable et al., 2011) for dry and semi-dry ecosystems such as the Loess Plateau in this study. 3) The significantly higher N content in the apple orchard soil resulted from high amount of N fertilization (300 *vs.* 160 kg N $ha^{-1}$) may be the third reason for to stimulate greater soil respiration rates. While this finding is consistent with Peng et al. (2010) in forest studies which showed that N fertilization increased soil respiration, it contradicts the results of Ramirez et al. (2010a, 2010b) and Janssens et al. (2010), both reporting an inhibited effect of N fertilization on soil microbial respiration. The inconsistency among these reports may be because there were more variables *in situ* field experiment in this study compared to those well controlled laboratory conditions in their studies. The higher soil N content in the apple orchard could further lead to a decrease in the C: N ratios, which may affect the soil C quality and enzyme activities (Table 2 and Fig. 7) (Tu et al.,

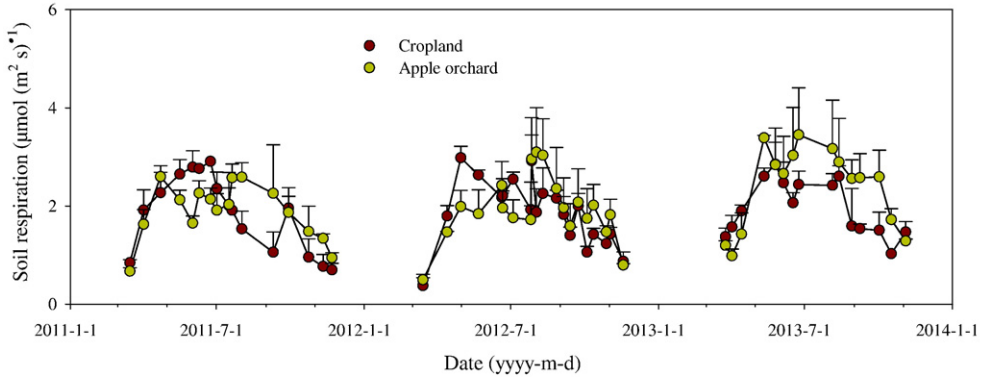


**Fig. 4.** Dynamics of soil respiration (μmol $m^{-2}$ $s^{-1}$) in the cropland and apple orchard over the experimental period from 2011 to 2013.

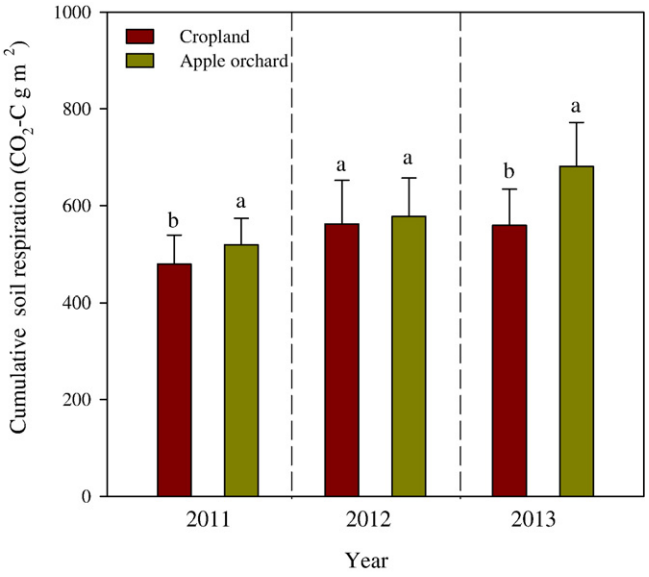


**Fig. 5.** Cumulative soil respiration ($CO_2$-C g $m^{-2}$) in the cropland and apple orchard.

2013; Zhang et al., 2014) and consequently had an impact on soil organic matter decomposition (Ball and Virginia, 2014; Unal et al., 2014). Apart from the above-discussed reasons, land use-induced differences in root biomass and substrate carbon input may also indirectly influence soil respiration (Lee and Jose, 2003; Wang et al., 2016). However, fine root biomass was no pronouncedly different between the two land use types in our study (orchard *vs.* cropland: 1.68 *vs.* 1.73 t $ha^{-1}$, not published), hence was considered not quite relevant in current study. Further research is required to effectively identify the relative contributions from microbial respiration and root respiration to soil $CO_2$ emission.

### 4.2. Changes in $Q_{10}$ induced by land use types

Unlike the greater soil respiration patterns observed in the apple orchard, the $Q_{10}$ values in the apple orchard was lower than that in the cropland soil (Table 3). This can partially be attributed to the lower soil moisture availability in the cropland that could increase $Q_{10}$ values by disconnecting soil pore water, thus slowing down the diffusion rate of solutes that contain extracellular enzymes produced by microorganisms and available substrates must occur in the liquid phase (Balogh et al., 2011; Davidson et al., 1998; Illeris et al., 2004; Wan et al., 2007). The similar result was also found by Gulledge and Schimel (2000), which pointed out that $Q_{10}$ values was larger in wet years than that in drought years. The lower C: N ratios in the apple orchard soil (6.5 *vs.* 8.4 in Table 2) also contributed to its lower $Q_{10}$ values, as the higher quality subtracts (lower C: N ratios in this study) was easy to be mineralized soil organic matter required lower activation energy for chemical and microbial decomposition (Leifeld and von Lutzow, 2014; Jiang et al., 2015; Wang et al., 2016). This is consistent with the enzyme-kinetic hypothesis proposed by Bosatta and Agren (1999) that degradation of high-quality substrate preformed a lower $Q_{10}$ value. Since no pronounced differences were found in $Q_{10}$ among roots biomass and root N concentration (Atkinson et al., 2007; Wang et al., 2016; Zhang et al., 2014), the responses of microbial respiration to temperature changes may be the major driver responsible for the $Q_{10}$ values variation in this study.

### 4.3. Potential role of bacterial community in soil respiration and $Q_{10}$

Soil temperature and soil moisture, SOC, total N and SMBC also showed the high Spearman's correlation ($p < 0.05$) with OTUs, diversity (Table 5). Our results are consistent with previous evidence that soil moisture and chemical constituents (*i.e.* C and N concentration) influenced bacteria communities (Romanowicz et al., 2016; Wang et al., 2016). However, since the soil temperature was not significantly different between the apple orchard and the cropland in this study, the shifts in microbial community composition could be largely attributed to the changes in soil moisture and nutrient availability (Table 2). The 28% greater soil moisture, 20% greater in total N concentration and 23% lower C: N ratios in the apple orchard probably contributed to its higher bacterial community diversity (Tables 2 and 5). Increasing soil water and nutrient can stimulate microbial respiration by increasing extracellular enzyme activities and the availability of substrates (Zhao et al., 2016).

The soil microbial population size (SMBC: 136 *vs.* 105 mg $kg^{-1}$) and extracellular enzymes (44.92 *vs.* 39.09 and 21.39 *vs.* 17.50 nmol $h^{-1}$ $g^{-1}$) (Table 2) may both contribute to the higher soil respiration in the apple orchard (Figs. 4 and 5). Furthermore, since the $CO_2$ respired is determined by the abundance of certain taxa, not by the overall diversity (Banerjee et al., 2016), the lower Acidobacteria, and the higher Bacteroidetes and Proteobacteria in the apple orchard was considered associated with its higher soil respiration (Figs. 4 and 5). This agrees with the findings reported by Fierer et al. (2007) and Thomson et al. (2010) that C mineralization rates was negatively associated with the abundances of Acidobacteria, but positively associated with the abundances of Betaproteobacteria and Bacteroidetes.

Furthermore, the different correlations between the relative abundances of microbial communities and the $Q_{10}$ values of the two land use types (Table 3 and Fig. 6) also suggest that land use induced variations in soil microbial communities could also influence their sensitivity to temperature changes. To be specific, the higher $Q_{10}$ values were observed to be correlated with the relative abundance of Proteobacteria and Bacteroidetes, and the lower $Q_{10}$ values related to Acidobacteria, Planctomycetes and Verrucomicrobia (Tables 3 and Fig. 6). Following previous reports, Proteobacteria and Bacteroidetes were classified as copiotrophs (Fierer et al., 2007), and Acidobacteria, Planctomycetes and Verrucomicrobia were classified as oligotrophs (Ramirez et al., 2010a, 2010b). Therefore, our findings jointly suggest that copiotrophic prokaryotes responded positively with high $Q_{10}$ values, and the oligotrophs showed a negative response to $Q_{10}$ values. Similar $Q_{10}$ association with trophic guilds was also observed in a 117-day incubation experiment in Bai et al. (2017). In addition, the variation of bacterial communities can also affect $Q_{10}$ values through extracellular enzyme. The genus encoding the β-glucosidase and cellobiohydrolase indicated that the apple orchard significantly increased the relative abundance of genus which could induce the β-glucosidase (8.88% *vs.* 8.19%) and

**Table 3**
The relationship between soil respiration and soil temperature (y-T) for each year from 2011 to 2013.

| Year | Land use type | Functions | $r^2$ | $p$ | $Q_{10}$ |
|---|---|---|---|---|---|
| 2011 | Cropland | $y = 0.913e^{0.0428T}$ | 0.66 | <0.01 | 1.53 |
| | Apple orchard | $y = 0.972e^{0.0383T}$ | 0.52 | <0.01 | 1.47 |
| 2012 | Cropland | $y = 0.919e^{0.0456T}$ | 0.85 | <0.01 | 1.58 |
| | Apple orchard | $y = 1.116e^{0.0345T}$ | 0.51 | <0.01 | 1.41 |
| 2013 | Cropland | $y = 0.882e^{0.0571T}$ | 0.65 | <0.01 | 1.77 |
| | Apple orchard | $y = 1.063e^{0.0299T}$ | 0.43 | <0.01 | 1.35 |

**Table 4**
Diversity indices at 97% sequence similarity of 16S rRNA gene sequence calculated based on 64,246 sequences for each sample in the cropland and apple orchard soils.

| Treatment | Chao1 estimator of richness | Observed species | Shannon's diversity index | OUT number |
|---|---|---|---|---|
| Cropland | 4481 ± 102b | 3997 ± 38b | 9.99 ± 0.02b | 4579 ± 73b |
| Orchard | 4983 ± 234a | 4364 ± 156a | 10.18 ± 0.03a | 5031 ± 233a |

Values with different letters in a column mean significant difference at $p < 0.05$, values are means of three replicates ± SE.

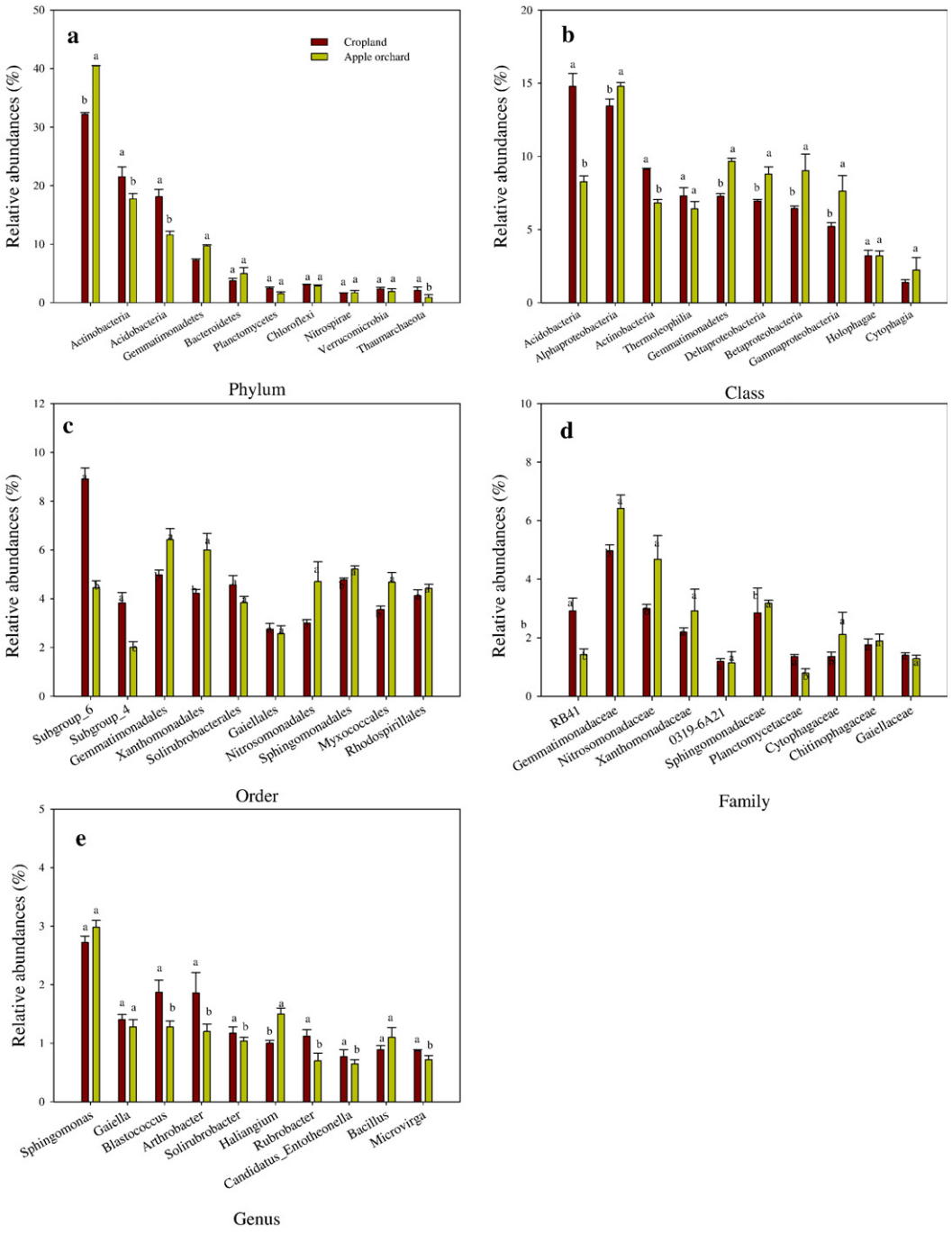


**Fig. 6.** Relative abundances of soil bacterial communities changed by land use at phylum, class, order, family, and genus levels.

**Table 5**
Spearman correlations of soil microbial diversity with Soil physical and chemical properties ($p < 0.05$).

| Soil characteristics | Chao1 estimator of richness | Observed species | Shannon's diversity index | OUT number |
|---|---|---|---|---|
| Total nitrogen (g $kg^{-1}$) | 0.943 | 0.943 | 0.771 | 0.921 |
| Soil organic carbon (SOC g $kg^{-1}$) | −0.721 | −0.771 | −0.695 | −0.657 |
| C: N ratios | −0.827 | −0.943 | −0.771 | −0.900 |
| Soil temperature (°C) | −0.829 | −0.794 | −0.943 | −0.771 |
| Soil moisture (WFPS%) | 0.691 | 0.771 | 0.600 | 0.714 |

cellobiohydrolase (0.75% *vs.* 0.71%) (Fig. 7). The β-glucosidase and cellobiohydrolase secreting by microbes are often associated with organic carbon catalytic (Amin et al., 2014; Dionisi et al., 2015). Hence, the greater enzyme content (Table 2) in the apple orchard soil could break down residues more easily to produce more readily available substances (Fierer et al., 2007; Gunina and Kuzyakov, 2015) with lower total activation energy (Shimizu et al., 1998; Grammelis et al., 2008; Baz et al., 2014), consequently leading to lower $Q_{10}$ values.

## 5. Conclusion

Different land use types may modify soil respiration and its sensitivity to temperature changes, yet their responses could be contrasting. Our observations suggest that, compared to the cropland, the apple

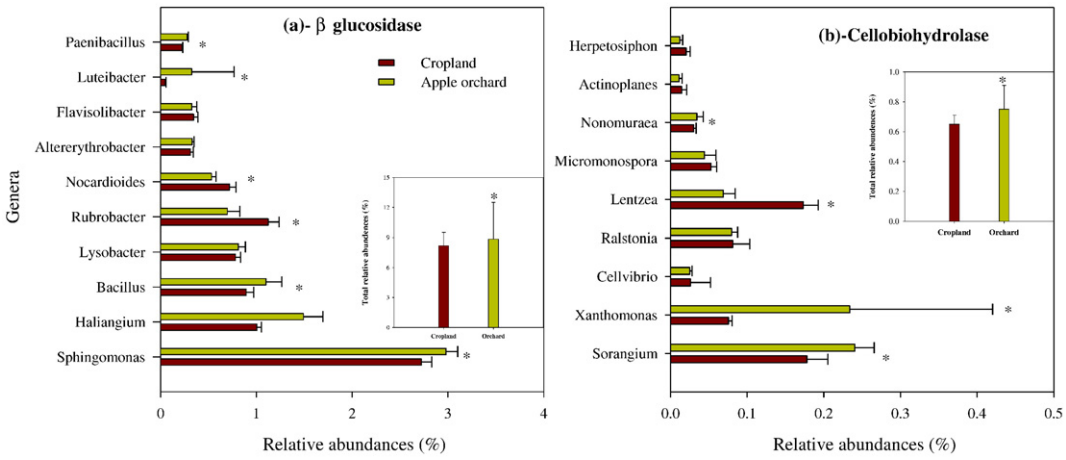


**Fig. 7.** Relative abundances of genera in bacterial. All the genera showed in this figure contain the genes which can encode the 3.2.1.21 and 3.2.1.91 (based on KEGG database, http://www.kegg.jp). * indicates the effect between cropland and apple orchard is significant.

orchard soil had a higher soil respiration and lower temperature sensitivity of soil respiration. The lower $Q_{10}$ in the apple orchard was mainly resulted from variation of bacterial community structure and β-glucosidase and cellobiohydrolase activity. The lower C: N ratios in the apple orchard also contributed to its lower $Q_{10}$. This brings about great uncertainties to the Chinese Loess Plateau, which is mainly a complex patchwork of fragmented landforms and land use types. The contrasting correlations of bacterial community and activities with soil respiration and $Q_{10}$ further highlight the necessity to take the possible effects of land use types on the soil respiration and its temperature sensitive into account when modeling regional C balances on the Chinese Loess Plateau and similar regions under future climate conditions.

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